Chapter 1

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- 1. Complex traits & QTL mapping
- look at Karl & Saunak's chapter 1
- goal is to motivate study of complex traits with QTL mapping

Identification of genes that contribute to measurable phenotypes has a long and successful history in model organisms. Complex traits include classical clinical phenotypes such as systolic blood pressure and body weight as well as newly measurable biomolecular phenotypes like gene expression levels, protein concentrations, and plasma lipid levels

Study of genetic contributions to complex traits has a long and rich history within statistical genetics.

- 2. Univariate QTL scan in two-parent crosses
- goal: explain a QTL "scan" in backcross & intercross. Use pictures/diagrams of chromosome(s)
- 3. Multivariate QTL scan in two-parent crosses
- 3.5 Testing pleiotropy v separate QTL in two-parent crosses
 - 4. Multiparental populations
 - what are they? Breeding design for CC & DO. Why use them?
 - 5. Univariate QTL mapping in MPP
 - contrast with univariate QTL mapping in two-parent crosses
 - 6. Multivariate mapping in mpp
 - 7. Testing pleiotropy vs separate QTL in MPP
 - 8. Testing pleiotropy vs separate QTL to dissect an expression trait hotspot Tian et al. 2016. ?Schadt et al. 2005?